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tcagtatgga ggattgtcaa ctactctcca tcacagcagt aggtgtgatg tagaagagtg 660
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             20   25   30

His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
         35   40   45

1

Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
    50   55   60

Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser
65   70   75   80

Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu
                85   90   95

Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr
            100   105   110

Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys
        115   120   125

Asp Tyr Val Tyr Lys Asp Met Ile Asp Phe Leu Asn Arg Phe Asn
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<212> DNA
<213> Catalpa sp.

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<213> Catalpa sp.

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Ile Glu Thr Pro Val His Met Ala Gln Thr Val Arg Tyr Gly Ile Leu
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Pro Lys Tyr Asp Tyr Gly Asn Pro Ser Phe Asn Leu Ala His Tyr Gly
            20   25   30

Glu Ser Arg Pro Pro Val Tyr Asp Leu Ser Lys Ile Pro Leu Asp Ile
            35   40   45

Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys
    50   55   60

Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys
65   70   75   80

Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile
                85   90   95

2

Gly Val Thr Ala Lys Asp Ile Val Tyr Asn Gln Ile Val Thr Phe Phe
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Arg Asn Gln Ala
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<213> Catalpa sp.

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            20   25   30

Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser
        35   40   45

Thr Ala Val Thr Val His Gly Tyr Lys Cys Gln Glu Phe Glu Val Thr
     50   55   60

Thr Asp Asp Gly Tyr Ile Leu Ser Val Gln Arg Ile Leu Glu Gly Arg
 65   70   75   80

Ala Gly Gly Gly Gly Pro Lys Arg Pro Pro Val Leu Leu Gln His Gly
                85   90   95

Val Leu Val Asp Gly Met Thr Trp Leu Val Asn Gly Pro Glu Gln Ser
            100   105   110

Leu Ala Met Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ser Asn
            115   120   125

Ile Arg Gly Thr Arg Phe Ser Arg Arg His Val Ser Leu Asp Pro Thr
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Asp Pro Glu Tyr Trp Asp Trp Ala Trp Asp Asp Leu Gly
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            20   25   30

Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg
        35   40   45

Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro
    50   55   60

Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu
65   70   75   80

Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro
                85   90   95

Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe
            100   105   110

Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly
            115   120   125

Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly
    130   135   140

His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp
145   150   155   160

Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr
            165   170   175

Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr
            180   185   190

Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile
        195   200   205

Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser
    210   215   220

Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu
225   230   235   240

Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val
                245   250   255

Gln Ile Leu Asp Ser Leu Cys Asp Asp Glu His Leu Asp Cys Asn Asp
            260   265   270

Leu Leu Ser Ser Ile Thr Val Lys Thr Val Val Gln Ser Ser
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atattagtga tgacaaatgc cccccacaac ctcatccctt angtatgtgc aggtcccgag   180
tagcagctta cggctatcca tgtgaggaat accatgtgac aacggaggat ggctacatcc   240
ttagcttaaa gaagatcccc tatggtctct ctggtgncac cganattacn agganaccgg   300
tactactgtt ccatgggcta ctggtggatg gtttctgttg ggtactgaac acaccaaaac   360
aatcactggg cttcacctgg ctgaangtgg tttgaaattt ggatcnccac tcncccgaaa   420
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Ala Cys Cys Leu Met Asn Leu Gln Ser Val Leu Ser Ser Ser Arg Met
             20                  25                  30

Arg Asn Thr Thr Asn Asp Ile Ser Asp Asp Lys Cys Pro Pro Gln Pro
             35                  40                  45
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His Pro Leu Xaa Met Cys Arg Ser Arg Val Ala Ala Tyr Gly Tyr Pro
    50                      55                  60

Cys Glu Glu Tyr His Val Thr Thr Glu Asp Gly Tyr Ile Leu Ser Leu
 65                  70                  75                      80

Lys Lys Ile Pro Tyr Gly Leu Ser Gly Xaa Thr Xaa Ile Thr Arg Xaa
                 85                  90                  95

Pro Val Leu Leu Phe His Gly Leu Leu Val Asp Gly Phe Cys Trp Val
             100             105                 110

Leu Asn Thr Pro Lys Gln Ser Leu Gly Phe Thr Trp Leu
         115                 120                 125
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             20   25   30

Gln Thr Gly Gln Lys Pro His Tyr Val Gly His Ser Met Gly Thr Leu
         35   40   45

Val Ala Leu Ala Ala Phe Ser Glu Gly Arg Val Val Ser Gln Leu Lys
     50   55   60

Ser Ala Ala Leu Leu Thr Pro Val Ala Tyr Leu Xaa His Xaa Asn Xaa
 65   70   75   80

Pro Asn Xaa Asn Pro Gly Trp Pro Xaa Arg
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9

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<212> PRT
<213> Oryza sativa

<400> 14

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                20                  25                  30

Ala Ala Ala Leu Arg Arg Val Gly Ser Gly Ser Gly Gly Leu Cys Asp
            35                  40                  45

Gln Leu Leu Leu Pro Leu Gly Tyr Pro Cys Thr Glu His Asn Val Glu
        50                  55                  60

Thr Lys Asp Gly Phe Leu Leu Ser Leu Gln His Ile Pro His Gly Lys
 65                  70                  75                  80

Asn Lys Ala Ala Asp Ser Thr Gly Pro Pro Val Phe Leu Gln His Gly
                85                  90                  95

Leu Phe Gln Gly Gly Asp Thr Trp Phe Ile Asn Ser Ala Glu Gln Ser
            100                 105                 110

Leu Gly Tyr Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Gly Asn
            115                 120                 125

Val Arg Gly Thr Arg Trp Ser Lys Gly His Ser Thr Phe Ser Val His
        130                 135                 140

Asp Lys Leu Phe Trp Asp Trp Ser Trp Gln Glu Leu Ala Glu Tyr Asp
145                 150                 155                 160
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Leu Leu Ala Met Leu Gly Tyr Val Tyr Thr Val Thr Gln Ser Lys Ile
                165   170   175

Leu Tyr Val Gly His Ser Gln Gly Thr Ile Met Gly Leu Ala Ala Leu
            180   185   190

Thr Met Pro Glu Ile Val Lys Met Ile Ser Ser Ala Ala Leu Leu Cys
            195   200   205

Pro Ile Ser Tyr Leu Asp His Val Ser Ala Ser Phe Val Leu Arg Ala
    210   215   220

Val Ala Met His Leu Asp Gln Met Leu Val Thr Met Gly Ile His Gln
225   230   235   240

Leu Asn Phe Arg Ser Asp Met Gly Val Gln Ile Val Asp Ser Leu Cys
            245   250   255

Asp Gly Glu His Val Asp Cys Asn Asn Leu Leu Ser Ala Ile Thr Gly
            260   265   270

Glu Asn Cys Cys Phe Asn Thr Ser Arg Ile Asp Tyr Tyr Leu Glu Tyr
            275   280   285

Glu Pro His Pro Ser Ser Thr Lys Asn Leu His His Leu Phe Gln Met
    290   295   300

Ile Arg Lys Gly Thr Phe Ala Lys Tyr Asp Tyr Gly Leu Leu Gly Asn
305   310   315   320

Leu Arg Arg Tyr Gly His Leu Arg Pro Pro Ala Phe Asp Leu Ser Ser
            325   330   335

Ile Pro Glu Ser Leu Pro Ile Trp Met Gly Tyr Gly Gly Leu Asp Ala
            340   345   350

Leu Ala Asp Val Thr Asp Val Gln Arg Thr Ile Arg Glu Leu Gly Ser
            355   360   365

Thr Pro Glu Leu Leu Tyr Ile Gly Asp Tyr Gly His Ile Asp Phe Val
    370   375   380

Met Ser Val Lys Ala Lys Asp Asp Val Tyr Val Asp Leu Ile Arg Phe
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<210> 16
<211> 80
<212> PRT
<213> Oryza sativa

<220>
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<222> (8)
<223> ANY AMINO ACID

<220>
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<222> (10)..(11)
<223> ANY AMINO ACID

<220>
<221> UNSURE
<222> (15)
<223> ANY AMINO ACID

<220>
<221> UNSURE
<222> (61)
<223> ANY AMINO ACID

<400> 16
Thr Ser Phe Thr Gly Lys Asn Xaa Cys Xaa Xaa Asn Ser Ala Xaa Asp
 1   5   10   15

Ile Phe Leu Lys Tyr Glu Pro Gln Pro Thr Ser Thr Lys Thr Leu Ile
            20   25   30

13

His Leu Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
        35   40   45

Val Met Pro Asp Ala Asn Val Ala Arg Tyr Gly Gln Xaa Asp Pro Pro
    50   55   60

Ala Tyr Asp Met Ala Ala Ile Pro Ala Trp Phe Pro Ile Phe Leu Ser
65   70   75   80

<210> 17
<211> 1718
<212> DNA
<213> Glycine max

<400> 17
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aatacattaa cacttcaatc ccacgctttc aatagataga tagagcattc attcatcacc  180
aacatggctc ttctaggctt aatgagtttt gctgccttga ccctttttctt ggtcctaaca  240
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gaggttacaa ctgatgatgg ttacattctg agcctgcaaa ggatcccaga aggtcgaggt  420
aaaagcagtg ggagtgggac aaggaagcaa ccagtggtta tacaacatgg agttcttgta  480
gatggtatga catggcttct aaacccacca gagcaagatc tgccgttgat tttagctgat  540
aatggatttg acgtgtggat tgcaaacaca agaggaacca gatatagtcg ccgacacatc  600
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ggccattcat tgggaacttt ggtagctttg gcatccttct cggaaggaaa attggttacc  780
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<210> 18
<211> 410
<212> PRT
<213> Glycine max

<400> 18
Met Ala Leu Leu Gly Leu Met Ser Phe Ala Ala Leu Thr Leu Phe Leu
1   5   10   15

Val Leu Thr Thr Val Pro Arg Gln Ala His Ala Ser Ser Arg Gly Asn
            20   25   30

Leu Gly Arg Asn Ile Asn Pro Ser Val Tyr Gly Ile Cys Ala Ser Ser
        35   40   45

14

```
Val Ile Val His Gly Tyr Lys Cys Gln Glu His Glu Val Thr Thr Asp
    50              55              60

Asp Gly Tyr Ile Leu Ser Leu Gln Arg Ile Pro Glu Gly Arg Gly Lys
 65              70              75                      80

Ser Ser Gly Ser Gly Thr Arg Lys Gln Pro Val Val Ile Gln His Gly
            85              90                  95

Val Leu Val Asp Gly Met Thr Trp Leu Leu Asn Pro Pro Glu Gln Asp
            100             105             110

Leu Pro Leu Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ala Asn
        115             120             125

Thr Arg Gly Thr Arg Tyr Ser Arg Arg His Ile Ser Leu Asp Pro Ser
    130             135             140

Ser Gln Ala Tyr Trp Asn Trp Ser Trp Asp Glu Leu Val Ser Tyr Asp
145             150             155             160

Phe Pro Ala Val Phe Asn Tyr Val Phe Ser Gln Thr Gly Gln Lys Ile
            165             170             175

Asn Tyr Val Gly His Ser Leu Gly Thr Leu Val Ala Leu Ala Ser Phe
        180             185             190

Ser Glu Gly Lys Leu Val Thr Gln Leu Lys Ser Ala Ala Leu Leu Ser
    195             200             205

Pro Ile Ala Tyr Leu Ser His Met Asn Thr Ala Leu Gly Val Val Ala
    210             215             220

Pro Lys Ser Phe Val Gly Glu Ile Thr Thr Leu Phe Gly Leu Ala Glu
225             230             235             240

Phe Asn Pro Lys Gly Leu Ala Val Asp Ala Phe Leu Lys Ser Leu Cys
            245             250             255

Ala His Pro Gly Ile Asp Cys Tyr Asp Leu Leu Thr Ala Leu Thr Gly
        260             265             270

Lys Asn Cys Cys Leu Asn Ser Ser Thr Val Asp Leu Phe Leu Met Asn
    275             280             285

Glu Pro Gln Ser Thr Ser Thr Lys Asn Met Val His Leu Ala Gln Thr
    290             295             300

Val Arg Leu Gly Ala Leu Thr Lys Phe Asn Tyr Val Arg Pro Asp Tyr
305             310             315             320

Asn Ile Met His Tyr Gly Glu Ile Phe Pro Pro Ile Tyr Asn Leu Ser
            325             330             335

Asn Ile Pro His Asp Leu Pro Leu Phe Ile Ser Tyr Gly Gly Arg Asp
        340             345             350

Ala Leu Ser Asp Val Arg Asp Val Glu Asn Leu Leu Asp Lys Leu Lys
        355             360             365
```

15

Phe His Asp Glu Asn Lys Arg Ser Val Gln Phe Ile Gln Glu Tyr Ala
    370   375   380

His Ala Asp Tyr Ile Met Gly Phe Asn Ala Lys Asp Leu Val Tyr Asn
385   390   395   400

Ala Val Leu Ser Phe Phe Asn His Gln Val
                405   410

<210> 19
<211> 1438
<212> DNA
<213> Glycine max

<400> 19
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caccaaaaac agcaacacag tttgtgtgaa gagctcatta tcccctacgg ttaccccctgc 180
tccgagcata cgattcaaac gaaggatggt ttcttgttag gtcttcaacg tgtctcttct 240
tcttcttctc ttcggcttcg gaaccatgga gatggaggcc ctccggttct gcttctgcat 300
ggattattca tggcaggtga tgcatggttt ctaaatactc cggaacaatc acttggcttc 360
atacttgcag atcatggttt tgatgtttgg gtaggaaacg tgcgtggaac acgctggagc 420
catggacata tatctttatt agagaagaaa aagcaatttt gggattggag ttggcaggaa 480
ttagccctgt atgatgttgc ggaaatgatc aattacatta attcagtaac aaactcaaag 540
atatttgtag ttgggcattc acaggggaca attatatctt tggctgcctt cactcaacca 600
gagatagtag aaaaggttga ggctgcagct cttctatctc caatatcata cttggatcat 660
gtcagtgcac ctcttgtact tagaatggtt aagatgcaca ttgatgagat gattcttacc 720
atgggcattc atcaactaaa cttcaaaagc gaatgggggg ccagtctctt ggtttcctta 780
tgtgataccc gcctaagttg caatgacatg ctttcatcca taacagggaa gaattgttgc 840
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atgattagtt ttttcaagtc atccggaaaa tttagtagta tgtaatgttt gcttccttcc 1260
ggtatgatgg atgtaattac tgtaatggtc tacgggtcca tctattactg cacttactgt 1320
aaagttgaaa tattaatatt ctgtggagtc caccttgatt ttctgtatgt atatatgatg 1380
acagatatat aaagatcggc gtcgcatgac ctgtttctgc aaaaaaaaaa aaaaaaa   1438

<210> 20
<211> 405
<212> PRT
<213> Glycine max

<400> 20
Met Arg Ile Gln Arg Phe Leu Ala Thr Leu Ala Ile Thr Val Ser Ile
  1   5   10   15

Leu Leu Gly Asn Gly Asn Pro Val Gln Cys Phe Asp Gly Gly Ser His
                20   25   30

Gln Lys Gln Gln His Ser Leu Cys Glu Glu Leu Ile Ile Pro Tyr Gly
            35   40   45

Tyr Pro Cys Ser Glu His Thr Ile Gln Thr Lys Asp Gly Phe Leu Leu
        50   55   60

Gly Leu Gln Arg Val Ser Ser Ser Ser Ser Leu Arg Leu Arg Asn His
  65   70   75   80

16

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Gly Asp Gly Gly Pro Pro Val Leu Leu Leu His Gly Leu Phe Met Ala
            85          90                      95

Gly Asp Ala Trp Phe Leu Asn Thr Pro Glu Gln Ser Leu Gly Phe Ile
            100             105             110

Leu Ala Asp His Gly Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr
            115             120             125

Arg Trp Ser His Gly His Ile Ser Leu Leu Glu Lys Lys Lys Gln Phe
    130             135             140

Trp Asp Trp Ser Trp Gln Glu Leu Ala Leu Tyr Asp Val Ala Glu Met
145             150             155             160

Ile Asn Tyr Ile Asn Ser Val Thr Asn Ser Lys Ile Phe Val Val Gly
            165             170             175

His Ser Gln Gly Thr Ile Ile Ser Leu Ala Ala Phe Thr Gln Pro Glu
            180             185             190

Ile Val Glu Lys Val Glu Ala Ala Ala Leu Leu Ser Pro Ile Ser Tyr
            195             200             205

Leu Asp His Val Ser Ala Pro Leu Val Leu Arg Met Val Lys Met His
    210             215             220

Ile Asp Glu Met Ile Leu Thr Met Gly Ile His Gln Leu Asn Phe Lys
225             230             235             240

Ser Glu Trp Gly Ala Ser Leu Leu Val Ser Leu Cys Asp Thr Arg Leu
            245             250             255

Ser Cys Asn Asp Met Leu Ser Ser Ile Thr Gly Lys Asn Cys Cys Phe
            260             265             270

Asn Glu Ser Arg Val Glu Phe Tyr Leu Glu Gln Glu Pro His Pro Ser
            275             280             285

Ser Ser Lys Asn Leu Asn His Leu Phe Gln Met Ile Arg Lys Gly Thr
    290             295             300

Tyr Ser Lys Tyr Asp Tyr Gly Lys Leu Lys Asn Leu Ile Glu Tyr Gly
305             310             315             320

Lys Phe Asn Pro Pro Lys Phe Asp Leu Ser Arg Ile Pro Lys Ser Leu
            325             330             335

Pro Leu Trp Met Ala Tyr Gly Gly Asn Asp Ala Leu Ala Asp Ile Thr
            340             345             350

Asp Phe Gln His Thr Leu Lys Glu Leu Pro Ser Pro Pro Glu Val Val
            355             360             365

Tyr Leu Glu Asn Tyr Gly His Val Asp Phe Ile Leu Ser Leu Gln Ala
    370             375             380

Lys Gln Asp Leu Tyr Asp Pro Met Ile Ser Phe Phe Lys Ser Ser Gly
385             390             395             400
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17

Lys Phe Ser Ser Met
                405

<210> 21
<211> 737
<212> DNA
<213> Zea mays

<400> 21
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tcccaagaac aatccgtgtg acccatcaga atgatattgt gccgcattta ccaccgtatt 180
attattacct aggtgaatgg acataccacc acttcgctag agaggtttgg cttcatgaga 240
gcatagatgg aaatgtagtt accagaaacg agacggtatg tgatgattct ggtgaagacc 300
cgacctgtag caggtcggtc tatgggatga gcgtagcaga tcatcttgag tactatgatg 360
tcacactaca tgctgattca agaggaacct gtcaattcgt gattggtgca gccaaccaag 420
tatacaacta cgttcgtgaa gttgatggat ccatcatcct gtcaagatac ccgcaagaac 480
cacaagctct agaatctatg tgactttgta tgccacggaa tgcacccctg tacagtattt 540
ttcattttca ttttgtgtac agctcatgaa atgctgggcg ctcctggagc tctccagagg 600
ataaggagag gctcaccttt ttaaatgtgc cccctttgct caagtgagaa tcgtgcatgt 660
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taaaaaaaaa aaaaaaa   737

<210> 22
<211> 166
<212> PRT
<213> Zea mays

<400> 22
Thr Arg Phe Cys Ala Leu Asp Leu Ser Val Lys Phe Gly Ser Gln Glu
  1   5   10   15

Val Glu Leu Met Thr Phe Gly Gln Pro Arg Ile Gly Asn Pro Ala Phe
                 20   25   30

Ala Val Tyr Phe Gly Glu Gln Val Pro Arg Thr Ile Arg Val Thr His
             35   40   45

Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Tyr Tyr Leu Gly
         50   55   60

Glu Trp Thr Tyr His His Phe Ala Arg Glu Val Trp Leu His Glu Ser
 65   70   75   80

Ile Asp Gly Asn Val Val Thr Arg Asn Glu Thr Val Cys Asp Asp Ser
                 85   90   95

Gly Glu Asp Pro Thr Cys Ser Arg Ser Val Tyr Gly Met Ser Val Ala
                100   105   110

Asp His Leu Glu Tyr Tyr Asp Val Thr Leu His Ala Asp Ser Arg Gly
             115   120   125

Thr Cys Gln Phe Val Ile Gly Ala Ala Asn Gln Val Tyr Asn Tyr Val
         130   135   140

Arg Glu Val Asp Gly Ser Ile Ile Leu Ser Arg Tyr Pro Gln Glu Pro
145   150   155   160

18

Gln Ala Leu Glu Ser Met
                    165

<210> 23
<211> 1434
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (226)
<223> n = A, C, G, or T

<220>
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<222> (315)
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<220>
<221> unsure
<222> (1306)
<223> n = A, C, G, or T

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<223> n = A, C, G, or T

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<222> (1359)
<223> n = A, C, G, or T

<220>
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<222> (1368)
<223> n = A, C, G, or T

<220>
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<222> (1373)
<223> n = A, C, G, or T

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tcttgctgtc tgctgcttct catggaagag agttgcctgt caagagtagt gaccgcagtt   180
ttatctacaa ccatactctt gcaaagacgc ttgtggaata tgcatnagcg gtgtatatga   240
cagatttaac cgctctgttt acgtggacat gctcaagatg caatgacttg actcaaggat   300
tcgagatgag atccntaatt gttgatgtgg agaaactgct tgcaggcatt gttggtgtag   360
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attggataaa agacttgata tggaagcagc ttgatctaag tnatccaaac atgccaaatg   480
caaaggtgca cagtggattt ttctcctcgt ataacaatac aattttgcgt ctagctatca   540
caagtgctgt gcacaaggca agaaagtcat atggagatat caatgtcata gtgacaggcc   600
actcgatggg aggagctatg gcttcttttt gcgcgctcga tcttgctatg aagcttggag   660
gtggcagtgt gcaactcatg acttttgggc agcctcgtgt tggcaatgct gcattcgcct   720
catacttcgc caaatatgta cccaacacaa ttcgagtgac acacgggcat gatattgtgc   780
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aggtatgggt ccaggattct gatggcaaca caactgaacg gatttgtgac gacagcggtg   900
aagacccaga ttgttgcagg tgcatctcca tgttcggctt gaggattcag gaccattcac   960

19

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ttacctagga gttgatatgg aagcggacga ctggagcacc tgtagaatca tcacagctca  1020
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gacgtctcca tcgttgaacc tagtgtacaa aacagattgg agcagttcta gataggcgga  1140
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gtcaaggaat aaatcgggag catctcttgt aacaaagaga tcaganatga tgtcataagg  1320
aaaatcatag gacgtttatg ctgattggna ggattgctnt ggtaatanat gancatgtaa  1380
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<210> 24
<211> 296
<212> PRT
<213> Zea mays

<220>
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<222> (50)
<223> ANY AMINO ACID

<220>
<221> UNSURE
<222> (80)
<223> ANY AMINO ACID

<220>
<221> UNSURE
<222> (129)
<223> ANY AMINO ACID

<400> 24

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 1               5              10                  15

Leu Ser Ala Ala Ser His Gly Arg Glu Leu Pro Val Lys Ser Ser Asp
            20              25                  30

Arg Ser Phe Ile Tyr Asn His Thr Leu Ala Lys Thr Leu Val Glu Tyr
        35              40                  45

Ala Xaa Ala Val Tyr Met Thr Asp Leu Thr Ala Leu Phe Thr Trp Thr
    50              55                  60

Cys Ser Arg Cys Asn Asp Leu Thr Gln Gly Phe Glu Met Arg Ser Xaa
65              70              75                  80

Ile Val Asp Val Glu Lys Leu Leu Ala Gly Ile Val Gly Val Asp His
            85              90                  95

Ser Leu Asn Ser Ile Ile Val Ala Ile Arg Gly Thr Gln Glu Asn Ser
            100             105             110

Val Gln Asn Trp Ile Lys Asp Leu Ile Trp Lys Gln Leu Asp Leu Ser
            115             120             125

Xaa Pro Asn Met Pro Asn Ala Lys Val His Ser Gly Phe Phe Ser Ser
    130             135             140

Tyr Asn Asn Thr Ile Leu Arg Leu Ala Ile Thr Ser Ala Val His Lys
145             150             155             160
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20

```
Ala Arg Lys Ser Tyr Gly Asp Ile Asn Val Ile Val Thr Gly His Ser
            165             170                 175

Met Gly Gly Ala Met Ala Ser Phe Cys Ala Leu Asp Leu Ala Met Lys
            180             185             190

Leu Gly Gly Gly Ser Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val
            195             200             205

Gly Asn Ala Ala Phe Ala Ser Tyr Phe Ala Lys Tyr Val Pro Asn Thr
    210             215             220

Ile Arg Val Thr His Gly His Asp Ile Val Pro His Leu Pro Pro Tyr
225             230             235             240

Phe Ser Phe Leu Pro Gln Leu Thr Tyr His His Phe Pro Arg Glu Val
            245             250             255

Trp Val Gln Asp Ser Asp Gly Asn Thr Thr Glu Arg Ile Cys Asp Asp
            260             265             270

Ser Gly Glu Asp Pro Asp Cys Cys Arg Cys Ile Ser Met Phe Gly Leu
    275             280             285

Arg Ile Gln Asp His Ser Leu Thr
    290             295
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<210> 25
<211> 1560
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (601)
<223> n = A, C, G, or T

<400> 25
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gcgtctccgc cgccgccgga tccggcgcga tgactactac ttggacgtgg agagcggcag   180
gcggcggtgc cgctggtgca gcagcagtac gtgaacgggc ggctcgtccg cctccgcacc   240
ttctccgtgt tcgaggtgag catgatggcc gccaagatcg cctacgagaa cgccgcctac   300
atcgagaacg tcgtcaacaa cgtctggaag ttccacttcg tggggttcta caactgctgg   360
aacaagttcg tgggcgacca cacgacgcag gcgttcgtgt tcaccgacaa ggcaagagga   420
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cacggacgta aacctgtcgt ggctgggcat gggcgagctg ggccacgtcc acgtcggctt   540
cctcaaggcg ctgggcctgc aggaggagga cggcaaggac gccacgcggg cgttccccaa   600
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ccagaagcag ctgcagaagc acccgaacgc caacgtcgtg gtcaccggcc acagcctcgg   720
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cgtctacttc gacggctggt acaagggccg cgagatcgcc aagggcggcg acgcgcccaa  1020
caagaactac ttcgacccca ggtacctgct gtccatgtac ggcaacgcgt gggggggacct  1080
cttcaagggc gccttcctgt gggccaagga gggcaaggac taccgcgagg cgccgtctc   1140
gctgctctac cgcgccaccg gcctgctcgt gcccggcatc gcgtcgcaca gcccccaggga  1200
ctacgtcaac gccgtccgcc tcggcagcgt cgcctcggcg tagcttttgg attgcatgtt  1260
cgtttccatg catgtgtatc attgcatgca ataattggat gaaataaaca gcaataagct  1320
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21

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tcatcagtat tattattgtt gttgttgaat atatgcatcc tctcctctct atatagaatt 1380
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aaaaaatgta tcaactgtga agcatatata tccatgcatg catgtgtgcc cgaaattttt 1500
gtttttaaaa aaaaaaaaaa aaaaaaaaac aaaaaaaaaa aaaaaacaaa aaaaaaaaaa 1560
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<210> 26
<211> 258
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (45)
<223> ANY AMINO ACID

<400> 26

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 1               5                   10                  15

Glu Leu Gly His Val His Val Gly Phe Leu Lys Ala Leu Gly Leu Gln
                20                  25                  30

Glu Glu Asp Gly Lys Asp Ala Thr Arg Ala Phe Pro Xaa Gly Ala Pro
            35                  40                  45

Asn Ala Val Pro Gly Lys Pro Leu Ala Tyr Tyr Ala Leu Arg Glu Glu
    50                  55                  60

Val Gln Lys Gln Leu Gln Lys His Pro Asn Ala Asn Val Val Val Thr
65                  70                  75                  80

Gly His Ser Leu Gly Ala Ala Leu Ala Thr Ile Phe Pro Ala Leu Leu
                85                  90                  95

Ala Phe His Gly Glu Arg Gly Val Leu Asp Arg Leu Leu Ser Val Val
            100                 105                 110

Thr Tyr Gly Gln Pro Arg Val Gly Asp Lys Val Phe Ala Gly Tyr Val
        115                 120                 125

Arg Ala Asn Val Pro Val Glu Pro Leu Arg Val Val Tyr Arg Tyr Asp
        130                 135                 140

Val Val Pro Arg Val Pro Phe Asp Ala Pro Pro Val Ala Asp Phe Ala
145                 150                 155                 160

His Gly Gly Thr Cys Val Tyr Phe Asp Gly Trp Tyr Lys Gly Arg Glu
                165                 170                 175

Ile Ala Lys Gly Gly Asp Ala Pro Asn Lys Asn Tyr Phe Asp Pro Arg
            180                 185                 190

Tyr Leu Leu Ser Met Tyr Gly Asn Ala Trp Gly Asp Leu Phe Lys Gly
            195                 200                 205

Ala Phe Leu Trp Ala Lys Glu Gly Lys Asp Tyr Arg Glu Gly Ala Val
        210                 215                 220

Ser Leu Leu Tyr Arg Ala Thr Gly Leu Leu Val Pro Gly Ile Ala Ser
225                 230                 235                 240
```

22

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His Ser Pro Arg Asp Tyr Val Asn Ala Val Arg Leu Gly Ser Val Ala
                245                250                255

Ser Ala


<210> 27
<211> 432
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (7)
<223> n = A, C, G, or T

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<220>
<221> unsure
<222> (105)
<223> n = A, C, G, or T

<220>
<221> unsure
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<222> (117)
<223> n = A, C, G, or T

<400> 27
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tttagcatcg ttcttgtgcc cttgacctct cttgttaagt atggatcgca ggaagttcaa 180
ctcatgactt ttggacagcc tcgggtaggc aatccttctt ttgctgcgta cttcagtgac 240
caagtcccga gaacaatccg tgtgacccat cagaatgaca ttgtcccaca cttgccacca 300
tatttttgct accttggcga atggacatat caccacttct cgagagaggt ttggcttcat 360
gagaccatag taggaaatgt agttactagg aatgagacca tctgtgatgg atcaggcgag 420
gacccaacat gc 432

<210> 28
<211> 106
<212> PRT
<213> Oryza sativa

<400> 28
Gly Pro Phe Ser Ile Val Leu Val Pro Leu Thr Ser Leu Val Lys Tyr
1   5   10   15

Gly Ser Gln Glu Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val Gly
            20   25   30

Asn Pro Ser Phe Ala Ala Tyr Phe Ser Asp Gln Val Pro Arg Thr Ile
        35   40   45

Arg Val Thr His Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Phe
    50   55   60

Cys Tyr Leu Gly Glu Trp Thr Tyr His His Phe Ser Arg Glu Val Trp
65   70   75   80

Leu His Glu Thr Ile Val Gly Asn Val Val Thr Arg Asn Glu Thr Ile
                85   90   95

Cys Asp Gly Ser Gly Glu Asp Pro Thr Cys
                100   105

<210> 29
<211> 1234
<212> DNA
<213> Glycine max

<400> 29
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ccacaaccca agtcttgatt gttttggaca agcatgagaa ccgcgatact tatgtggtag 120
ctttccgagg aacggaaccc tttgatgcag atgcatggtg cactgacctt gacatctcat 180
ggtacgcatt cccggcattg gaaaaatgca tggtggcttc atgaaagcct tagggctaca 240
gaaaaatgtg gggtggccta aggagattca aagggatgaa aatcttcccc cgttggccta 300
ctatgttatt agggacattc taaggaaagg tttgagtgaa aatcctaatg caaagtttat 360
cattacgggt catagtttgg gtggagcact cgcaatcttg taccctacga tcatgttctt 420
gcatgatgag aagttgctga ttgagaggtt ggaagggatc tacacgtttg gcaaccaag 480
agttggagat gaagcatatg cacagtatat gagacaaaaa ttgagggaaa attctatcag 540
gtattgcagg tttgtttatt gcaatgacat agttccgagg ttgccctatg atgataagga 600
cttgctcttc aagcactttg ggatctgcct tttctttaac aggcgctatg aactcaggat 660
tctcgaagaa gagccgaata agaactattt ctcgccatgg tgtgtgatac ccatgatgtt 720
caatgctgtt ttggaactaa taaggagctt taccatagcg tacaaaaatg gacctcacta 780
tagagaagga tggtttctct ttagtttcag gttggttggt ctgctgattc ctggcttacc 840

24

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tgctcacggt ccacaagatt atattaattc cactcttctg ggatcaattg aaaaacattt  900
taaagcagat tgatgtgtcc gtatacatga tcattccata ccactacgta catgtgtatg  960
gtcatgcaga ctaaaattta cataatcaag atttttagtt ttagaaaaaa tggtaataac 1020
acttgattat gtatcatgtg aagaatagtt atgtatcata atgatcatga ataatataac 1080
agtttgtcgt cagtacgagt tattgtatag taattaataa gctaggttta aagttgtttc 1140
ctttggtgca tggatttatc attaatgaga tcaatgtgaa gtttgtttat ttcaaaaaaa 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                              1234
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<210> 30
<211> 246
<212> PRT
<213> Glycine max

<400> 30

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His Leu Met Val Arg Ile Pro Gly Ile Gly Lys Met His Gly Gly Phe
  1               5                  10                  15

Met Lys Ala Leu Gly Leu Gln Lys Asn Val Gly Trp Pro Lys Glu Ile
             20                  25                  30

Gln Arg Asp Glu Asn Leu Pro Pro Leu Ala Tyr Tyr Val Ile Arg Asp
         35                  40                  45

Ile Leu Arg Lys Gly Leu Ser Glu Asn Pro Asn Ala Lys Phe Ile Ile
     50                  55                  60

Thr Gly His Ser Leu Gly Gly Ala Leu Ala Ile Leu Tyr Pro Thr Ile
 65                  70                  75                  80

Met Phe Leu His Asp Glu Lys Leu Leu Ile Glu Arg Leu Glu Gly Ile
                 85                  90                  95

Tyr Thr Phe Gly Gln Pro Arg Val Gly Asp Glu Ala Tyr Ala Gln Tyr
             100                 105                 110

Met Arg Gln Lys Leu Arg Glu Asn Ser Ile Arg Tyr Cys Arg Phe Val
         115                 120                 125

Tyr Cys Asn Asp Ile Val Pro Arg Leu Pro Tyr Asp Asp Lys Asp Leu
     130                 135                 140

Leu Phe Lys His Phe Gly Ile Cys Leu Phe Phe Asn Arg Arg Tyr Glu
145                 150                 155                 160

Leu Arg Ile Leu Glu Glu Glu Pro Asn Lys Asn Tyr Phe Ser Pro Trp
                 165                 170                 175

Cys Val Ile Pro Met Met Phe Asn Ala Val Leu Glu Leu Ile Arg Ser
             180                 185                 190

Phe Thr Ile Ala Tyr Lys Asn Gly Pro His Tyr Arg Glu Gly Trp Phe
             195                 200                 205

Leu Phe Ser Phe Arg Leu Val Gly Leu Leu Ile Pro Gly Leu Pro Ala
     210                 215                 220

His Gly Pro Gln Asp Tyr Ile Asn Ser Thr Leu Leu Gly Ser Ile Glu
225                 230                 235                 240
```

25

Lys His Phe Lys Ala Asp
                245

<210> 31
<211> 490
<212> DNA
<213> Glycine max

<400> 31
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ctccataagg gatttgctaa agaagtgttt gaatagaaat gataaagcaa agtttattct 120
tacgggtcat agtcttggtg gagcacttgc aattcttttt cccgctatgc taattttgca 180
tgctgagaca tttcttttgg aaaggcttga aggggtgtac acatttggac agcctagggt 240
tggagatgaa acatttgcta aatacatgga aaatcaattg aaacattatg gcattaagta 300
ttttaggttt gtttactgca acgatattgt tcctaggttg ccctttgatg aagatatcat 360
gaaatttgag cattttggga catgtcttta ttatgacagg agctatacat gcaaggtaca 420
tatataagta tttaattttt ttgattcatg catatattcg tcattgtaat caacttttttt 480
ttttctgggg   490

<210> 32
<211> 141
<212> PRT
<213> Glycine max

<400> 32
His Glu Glu Arg Trp Pro Lys Glu Ile Glu Thr Asp Glu Asn Arg Pro
  1   5   10   15

Arg Val Tyr Tyr Ser Ile Arg Asp Leu Leu Lys Lys Cys Leu Asn Arg
             20   25   30

Asn Asp Lys Ala Lys Phe Ile Leu Thr Gly His Ser Leu Gly Gly Ala
         35   40   45

Leu Ala Ile Leu Phe Pro Ala Met Leu Ile Leu His Ala Glu Thr Phe
     50   55   60

Leu Leu Glu Arg Leu Glu Gly Val Tyr Thr Phe Gly Gln Pro Arg Val
 65   70   75   80

Gly Asp Glu Thr Phe Ala Lys Tyr Met Glu Asn Gln Leu Lys His Tyr
                 85   90   95

Gly Ile Lys Tyr Phe Arg Phe Val Tyr Cys Asn Asp Ile Val Pro Arg
             100   105   110

Leu Pro Phe Asp Glu Asp Ile Met Lys Phe Glu His Phe Gly Thr Cys
             115   120   125

Leu Tyr Tyr Asp Arg Ser Tyr Thr Cys Lys Val His Ile
     130   135   140

<210> 33
<211> 774
<212> DNA
<213> Triticum aestivum

<400> 33
gcacgagaat attcccatca tggtgacagg acattccatg ggagggggcca tggcttcgtt 60
ttgtgccctt gatcttattg tcaactatgg gttaaaggac gtgaccctgc tgacatttgg 120

26

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gcaacctcgg attggtaatg ctgtgtttgc tacccacttt aagaaatact tgccaaacgc 180
aattcgagtt accaacgcac atgatattgt gcctcatcta cccccgtact accagtactt 240
cccacagaat acctaccatc atttcccacc agaggtttgg gttcataaca ttggactcga 300
tagcctacta tacccgatcg agcacatctg tgatcattct ggagaaagac cccacttgca 360
gcaggccctt ggttggaaat agcgtccagg cccatacccc ctttcttggc tccagcatcc 420
atcccgagtc gcgcggatca tccagaatcg tcacggatga caatatgctc aggcacaaag 480
ttgcccctgt agacggtgtt attgtcttct cgaagcagcc tggtttatca gttggtcagc 540
tactcagtac acagtaaaca agctcaagat tacatggatt tattttgatg ttttttttttg 600
ccaaagaaca atattcttgt tggcaatcaa agcactatct catgtatata tacgcgtgtg 660
atcctggctg gattaaatta tcctagctga gggtgtattt ctgaaatgta caaacatatc 720
tatgctgatt aaaaaaaaaa aaaaaaatac ttgaggcggc cccgtaccaa aaat      774
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<210> 34
<211> 126
<212> PRT
<213> Triticum aestivum

<400> 34

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His Glu Asn Ile Pro Ile Met Val Thr Gly His Ser Met Gly Gly Ala
 1               5                  10                  15

Met Ala Ser Phe Cys Ala Leu Asp Leu Ile Val Asn Tyr Gly Leu Lys
            20                  25                  30

Asp Val Thr Leu Leu Thr Phe Gly Gln Pro Arg Ile Gly Asn Ala Val
        35                  40                  45

Phe Ala Thr His Phe Lys Lys Tyr Leu Pro Asn Ala Ile Arg Val Thr
    50                  55                  60

Asn Ala His Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Gln Tyr Phe
65                  70                  75                  80

Pro Gln Asn Thr Tyr His His Phe Pro Pro Glu Val Trp Val His Asn
                85                  90                  95

Ile Gly Leu Asp Ser Leu Leu Tyr Pro Ile Glu His Ile Cys Asp His
            100                 105                 110

Ser Gly Glu Arg Pro His Leu Gln Gln Ala Leu Gly Trp Lys
            115                 120                 125
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<210> 35
<211> 398
<212> PRT
<213> Canis familiaris

<400> 35

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Met Trp Leu Leu Leu Thr Ala Ala Ser Val Ile Ser Thr Leu Gly Thr
 1               5                  10                  15

Thr His Gly Leu Phe Gly Lys Leu His Pro Thr Asn Pro Glu Val Thr
            20                  25                  30

Met Asn Ile Ser Gln Met Ile Thr Tyr Trp Gly Tyr Pro Ala Glu Glu
            35                  40                  45

Tyr Glu Val Val Thr Glu Asp Gly Tyr Ile Leu Gly Ile Asp Arg Ile
    50                  55                  60
```

27

Pro Tyr Gly Arg Lys Asn Ser Glu Asn Ile Gly Arg Arg Pro Val Ala
65   70   75   80

Phe Leu Gln His Gly Leu Leu Ala Ser Ala Thr Asn Trp Ile Ser Asn
            85   90   95

Leu Pro Asn Asn Ser Leu Ala Phe Ile Leu Ala Asp Ala Gly Tyr Asp
            100   105   110

Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ala Arg Arg Asn Leu
            115   120   125

Tyr Tyr Ser Pro Asp Ser Val Glu Phe Trp Ala Phe Ser Phe Asp Glu
    130   135   140

Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asp Phe Ile Leu Lys Lys
145   150   155   160

Thr Gly Gln Asp Lys Leu His Tyr Val Gly His Ser Gln Gly Thr Thr
                165   170   175

Ile Gly Phe Ile Ala Phe Ser Thr Asn Pro Lys Leu Ala Lys Arg Ile
            180   185   190

Lys Thr Phe Tyr Ala Leu Ala Pro Val Ala Thr Val Lys Tyr Thr Glu
        195   200   205

Thr Leu Leu Asn Lys Leu Met Leu Val Pro Ser Phe Leu Phe Lys Leu
    210   215   220

Ile Phe Gly Asn Lys Ile Phe Tyr Pro His His Phe Phe Asp Gln Phe
225   230   235   240

Leu Ala Thr Glu Val Cys Ser Arg Glu Thr Val Asp Leu Leu Cys Ser
            245   250   255

Asn Ala Leu Phe Ile Ile Cys Gly Phe Asp Thr Met Asn Leu Asn Met
            260   265   270

Ser Arg Leu Asp Val Tyr Leu Ser His Asn Pro Ala Gly Thr Ser Val
        275   280   285

Gln Asn Val Leu His Trp Ser Gln Ala Val Lys Ser Gly Lys Phe Gln
    290   295   300

Ala Phe Asp Trp Gly Ser Pro Val Gln Asn Met Met His Tyr His Gln
305   310   315   320

Ser Met Pro Pro Tyr Tyr Asn Leu Thr Asp Met His Val Pro Ile Ala
            325   330   335

Val Trp Asn Gly Gly Asn Asp Leu Leu Ala Asp Pro His Asp Val Asp
            340   345   350

Leu Leu Leu Ser Lys Leu Pro Asn Leu Ile Tyr His Arg Lys Ile Pro
        355   360   365

Pro Tyr Asn His Leu Asp Phe Ile Trp Ala Met Asp Ala Pro Gln Ala
    370   375   380

28

Val Tyr Asn Glu Ile Val Ser Met Met Gly Thr Asp Asn Lys
385   390   395

<210> 36
<211> 403
<212> PRT
<213> Caenorhabditis elegans

<400> 36
Met Trp Arg Phe Ala Val Phe Leu Ala Ala Phe Phe Val Gln Asp Val
 1   5   10   15

Val Gly Ser His Gly Asp Pro Glu Leu His Met Thr Thr Pro Gln Ile
            20   25   30

Ile Glu Arg Trp Gly Tyr Pro Ala Met Ile Tyr Thr Val Ala Thr Asp
        35   40   45

Asp Gly Tyr Ile Leu Glu Met His Arg Ile Pro Phe Gly Lys Thr Asn
    50   55   60

Val Thr Trp Pro Asn Gly Lys Arg Pro Val Val Phe Met Gln His Gly
65   70   75   80

Leu Leu Cys Ala Ser Ser Asp Trp Val Val Asn Leu Pro Asp Gln Ser
                85   90   95

Ala Gly Phe Leu Phe Ala Asp Ala Gly Phe Asp Val Trp Leu Gly Asn
            100   105   110

Met Arg Gly Asn Thr Tyr Ser Met Lys His Lys Asp Leu Lys Pro Ser
        115   120   125

His Ser Ala Phe Trp Asp Trp Ser Trp Asp Glu Met Ala Thr Tyr Asp
    130   135   140

Leu Asn Ala Met Ile Asn His Val Leu Glu Val Thr Gly Gln Asp Ser
145   150   155   160

Val Tyr Tyr Met Gly His Ser Gln Gly Thr Leu Thr Met Phe Ser His
            165   170   175

Leu Ser Lys Asp Asp Gly Ser Phe Ala Lys Lys Ile Lys Lys Phe Phe
        180   185   190

Ala Leu Ala Pro Ile Gly Ser Val Lys His Ile Lys Gly Phe Leu Ser
        195   200   205

Phe Phe Ala Asn Tyr Phe Ser Leu Glu Phe Asp Gly Trp Phe Asp Ile
    210   215   220

Phe Gly Ala Gly Glu Phe Leu Pro Asn Asn Trp Ala Met Lys Leu Ala
225   230   235   240

Ala Lys Asp Ile Cys Gly Gly Leu Lys Val Glu Ala Asp Leu Cys Asp
            245   250   255

Asn Val Leu Phe Leu Ile Ala Gly Pro Glu Ser Asp Gln Trp Asn Gln
            260   265   270

29

```
Thr Arg Val Pro Val Tyr Ala Thr His Asp Pro Ala Gly Thr Ser Thr
        275             280             285

Gln Asn Ile Val His Trp Met Gln Met Val His His Gly Gly Val Pro
        290             295             300

Ala Tyr Asp Trp Gly Thr Lys Thr Asn Lys Lys Lys Tyr Gly Gln Ala
305             310             315             320

Asn Pro Pro Glu Tyr Asp Phe Thr Ala Ile Lys Gly Thr Lys Ile Tyr
            325             330             335

Leu Tyr Trp Ser Asp Ala Asp Trp Leu Ala Asp Thr Pro Asp Val Pro
            340             345             350

Asp Tyr Leu Leu Thr Arg Leu Asn Pro Ala Ile Val Ala Gln Asn Asn
        355             360             365

His Leu Pro Asp Tyr Asn His Leu Asp Phe Thr Trp Gly Leu Arg Ala
    370             375             380

Pro Asp Asp Ile Tyr Arg Pro Ala Ile Lys Leu Cys Thr Asp Asp Tyr
385             390             395             400

Leu Gly Lys
```